

(5') 1 SDLEQERRAKEKLQEQQ
18 SDLEQDRLAKEKLQEQQ
35 SDLEQERLAKEKLQEQQ
52 SDLEQERRAKEKLQEQQ
69 SDLEQERRAKEKLQEQQ
86 SDLEQDRLAKEKLQEQQ
103 SDLEQERRAKEKLQEQQ
120 SDLEQERKAKEKLQEQQ
137 SDLEQERLAKEKLQEQQ
154 SDLEQERRAKEKLQEQQ
171 SDLEQERRAKEKLQEQQ
188 SDLEQERRAKEKLQEQQ
205 RDLEQ

210 RKADTKKNLERKKEHGDILAEDLYGRLEIP
240 AIELPSENERGYYPHQSSLPQDNRGNSRD
270 SKEISIIIEKTNRESITTNVEGRRDIHKGHL
300 EEKKGDSIKPEQKEDKS 316 (3')

FIGURE 1

0983744-044901

(5') 1 AAAGCGATCTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 52 AAAGCGATTTAGAACAAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
 103 AAAGCGATTTAGAACAAAGAGAGACTTGCTAAAGAAAAGTTGCAAGAACAAAC
 154 AAAGCGATCTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 205 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 256 AAAGCGATTTAGAACAAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC
 307 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 358 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 409 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 460 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 511 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAAC
 562 AAAGCGATTTAGAACAAAGAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC
 613 AAAGAGATTTAGAACAA
 630 AGGAAGGCTGATACGAAAAAATTTAGAAAGAAAAGGAACATGGAGAT
 681 ATATTAGCAGAGGATTTATATGTCGTTTAGAAAATACCAGCTATAGAACTT
 732 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTACCT
 783 CAGGACAACAGAGGGAATAGTAGAGATTCAGGAAATATCTATAATAGAA
 834 AAACAAATAGAGAAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
 885 CATAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA
 936 AAAGAAGATAAATCT 950 (3')

FIGURE 2

RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVKSVQEQQ
HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI
ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE
ESVAPSVEESVAEMLKER

FIGURE 3

TO THE "442860"

5' GAA TTC CGT GAT GAA CTT TTT AAT GAA TTA TTA AAT AGT GTA GAT
GTT AAT GGA GAA GTA AAA AAT ATT TTG GAG GAA AGT CAA GTT AAT
GAG GAT ATT TTT AAT AGT TTA GTA AAA AGT GTT CAA CAA GAA CAA CAA
CAC AAT GTT GAA GAA AA AGT TGA AGA AAG TGT AGA AGA AA ATG ACG
AAG AAA GTG TAG AAG AAA ATG TAG AAG AAA ATG AAG AAA ATG
ACG ACG GAA GTG TAG CCT CAA GTG TTG AAG AAA GTA TAG CTT CAA GTG
TTG ATG AAA GTA TAG ATT CAA GTA TTG AAG AAA ATG TAG CTC CAA CTG
TTG AAG AAA TCG TAG CTC CAA CTG TTG AAG AAA TTG TAG CTC CAA GTG
TTG TAG AAA AGT GTG CTC CAA GTG TTG AAG AAA GTG TAG CTC CAA GTG
TTG AAG AAA GTG TAG CTG AAA TGT TGA AGG AAA GGA ATT C 3'

FIGURE 4

TOBTHO"HEE2E860

TO: "THE" 106

| | |
|---|------------------|
| <u>NSRDSKEISIIIEKTNRESITTNVEGRRDIHK</u> | <u>LSA-TER</u> |
| <u>DELFNELLNSVDVNGEVKENILEESQ</u> | <u>729S-NRI</u> |
| <u>LEESQVNDIDFSNSLVKSVQEQQHNV</u> | <u>729S-NRII</u> |
| <u>VEKCAPSVEESVAPSVESVAEMLKER</u> | <u>729S-Rep</u> |

FIGURE 5

NUCLEOTIDE SEQUENCE OF THE LSA GENE
5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

33 ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG
84 ATATTTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATCA
135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA
186 GGAAAATCACGAGAAGAAACACGTTTTATCTCATAATTCATATGAGAAAAC
237 AAAAATAATGAAAATAATAAATTTTTCGATAAGGATAAAGAGTTAACGATGT
288 CTAATGTAAAAAATGTGTCAACAAACAAATTTCAAAGTCTTTTAAGAAATCT
339 TGGTGTTCAGAGAATATATTCCTTAAAGAAAATAAATTAATAAGGAAGGG
390 AAATTAATTGAACACATAATAAATGATGATGACGATAAAAAAAAAATATATTA
441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAAGCA

(CODING 5' END, repetitive)

492 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTGAGAACAAGAGAGACGT
543 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
594 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
645 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
696 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
747 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
798 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
849 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTT
900 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988

FIGURE 6

DNA sequence 956 b.p. ATGAACATATT ... AAGGATTTAGA linear

FIGURE 7A

FIGURE 7B

| | | |
|---|-----------|--|
| 781 / 261 | 811 / 271 | |
| CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG | | |
| gln glu gln gln ser asp leu leu glu gln glu arg leu ala lys glu lys leu gln glu gln | | |
| 841 / 281 | 871 / 291 | |
| CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT | | |
| gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp | | |
| 901 / 301 | 931 / 311 | |
| TTA GAA CAA GAG AGA CGT GCT GCT AAA GAA AGG TTG CAA GAA CAA CAA AGC GAT TTA | | |
| leu glu gln glu arg arg ala lys glu arg leu gln glu gln gln ser asp leu | | |

FIGURE 7C

NUCLEOTIDE SEQUENCE OF THE LSA GENE
3' END

(CODING 3' END, REPETITIVE)

1 CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
37 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
88 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT
139 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
190 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
241 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT
343 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
445 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
496 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
598 GCTAAAGAAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

(CODING 3' END, UNIQUE)

640 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
691 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
793 CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
844 AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
895 CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA
946 AAAGAAGATAAATCTGCTGACATACAAAATCATACTTAGAGACAGTAAAT
997 ATTTCTGATGTTAATGATTTTTCAAATAAGTAAGTATGAGGATGAAATAAGT
1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT
1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA
1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT
1201 TAGATGATTTAGATGAAGGAATAGAAAAATCATCAGAAGAATTATCTGAAG
1252 AAAAAATAAAAAAAGGAAAGAAATATGAAAAACAAAGGATAATAATTTTA
1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAATAAAATATAAAATG
1354 ATAAGCAGGTTAATAAGGAAAAGGAAAAATTCATAAAATCATTGTTTCATA
1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG
1456 ATATAACTAAATATTTTATGAACTATAA (stop)

(NON-CODING 3' END)

1485 AAGGTTATATATTT 1498

FIGURE 8

093744-442860

LSA.3'.ALL -> 1-phase Translation

DNA sequence 1496 b.p. CAAGAACAACAA ... GGTTATATATTT linear

| | | |
|---|-----------|--|
| 1 / 1 | 31 / 11 | |
| CAA GAA CAA CAA AGC GAT CTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA | | |
| gln glu gln gln ser asp leu glu gln glu arg ala lys glu lys leu gln glu gln | | |
| 61 / 21 | 91 / 31 | |
| CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA AAG TTA CAA GAG CAG CAA AGC GAT | | |
| gln ser asp leu glu gln asp arg leu ala lys glu lys leu gln glu gln gln ser asp | | |
| 121 / 41 | 151 / 51 | |
| TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT CTA GAA CAA | | |
| leu glu gln glu arg leu ala lys glu lys leu gln glu gln ser asp leu glu gln | | |
| 181 / 61 | 211 / 71 | |
| GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAG AGA CGT | | |
| glu arg arg ala lys glu lys leu gln glu gln ser asp leu glu gln glu arg arg | | |
| 241 / 81 | 271 / 91 | |
| GCT AAA GAA AAG TTG CAA GAA CAA AGC GAT TTA GAA CAA GAT AGA CTT GCT AAA GAA | | |
| ala lys glu lys leu gln glu gln ser asp leu glu gln asp arg leu ala lys glu | | |
| 301 / 101 | 331 / 111 | |
| AAG TTA CAA GAG CAG CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA | | |
| lys leu gln glu gln ser asp leu glu gln glu arg ala lys glu lys leu gln | | |

FIGURE 9A

| | | | |
|---|---|-----------|---|
| 361 / 121 | GAA CAA AGC GAT TTA GAA AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA | 391 / 131 | GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA |
| glu gln gln 421 / 141 | ser asp leu glu gln gln gln gln gln gln gln gln gln gln gln gln gln | 451 / 151 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA CAA CAA CAA | ser asp leu glu gln gln gln gln gln gln gln gln gln gln gln gln | 511 / 171 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| 481 / 161 | GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA CAA CAA CAA CAA | 571 / 191 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| glu gln gln 541 / 181 | AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA CAA CAA CAA | 631 / 211 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| AGA CGT GCT AAA GAA AAG TTG CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA | arg arg ala lys glu gln gln gln gln gln gln gln gln gln gln gln gln | 691 / 231 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| 601 / 201 | AAA GAA AAG TTG CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA CAA CAA | 751 / 251 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| lys glu lys 661 / 221 | AAT TTA GAA AGA CGT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT | 811 / 271 | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| asn leu glu 721 / 241 | GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT | | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| 781 / 261 | TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA | | glu gln gln gln gln gln gln gln gln gln gln gln gln gln gln gln |
| ser ser leu | ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile | | ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile |

FIGURE 9B

| | | |
|---|---|--|
| 841 / 281 | 871 / 291 | |
| GAA AAA ACA AAT AGA GAA TCT ATT ACA | ACA AAT GTT GAA GGA CGA AGG GAT ATA CAT AAA | |
| glu lys thr asn arg glu ser ile thr thr | thr asn val glu gly arg asp ile his lys | |
| 901 / 301 | 931 / 311 | |
| GGA CAT CTT GAA GAA AAG AAA GAT GGT TCA ATA AAA CCA GAA CAA AAA GAT AAA TCT | | |
| gly his leu glu glu lys lys asp gly ser ile lys pro glu gln lys glu asp lys ser | | |
| 961 / 321 | 991 / 331 | |
| GCT GAC ATA CAA AAT CAT ACA TTA GAG ACA GTA AAT ATT TCT GAT GTT AAT GAT TTT CAA | | |
| ala asp ile gln asn his thr leu glu thr val asn ile ser asp val asn asp phe gln | | |
| 1021 / 341 | 1051 / 351 | |
| ATA AGT AAG TAT GAG GAT GAA ATA AGT GCT GAA TAT GAC GAT TCA TTA ATA GAT GAA GAA | | |
| ile ser lys tyr glu asp glu ile ser ala glu tyr asp ser leu ile asp glu glu | | |
| 1081 / 361 | 1111 / 371 | |
| GAA GAT GAT GAA GAC TTA GAC GAA TTT AAG CCT ATT GTG CAA TAT GAC AAT TTC CAA GAT | | |
| glu asp asp glu asp leu asp glu phe lys pro ile val gln tyr asp asn phe gln asp | | |
| 1141 / 381 | 1171 / 391 | |
| GAA GAA AAC ATA GGA ATT TAT AAA GAA CTA GAA GAT TTG ATA GAG AAA AAT GAA AAT TTA | | |
| glu glu asn ile gly ile tyr lys glu leu glu asp leu ile glu lys asn glu asn leu | | |
| 1201 / 401 | 1231 / 411 | |
| GAT GAT TTA GAT GAA GGA ATA GAA AAA TCA TCA GAA GAA TTA TCT GAA GAA AAA ATA AAA | | |
| asp asp leu asp glu gly ile glu lys ser ser glu glu leu ser glu glu lys ile lys | | |

FIGURE 9C

1261 / 421 1291 / 431
 AAA GGA AAG AAA TAT GAA AAA ACA AAG GAT AAT AAT TTT AAA CCA AAT GAT AAA AGT TTG
 lys gly lys lys tyr glu lys thr lys asp asn phe lys pro asn asp lys ser leu
 1321 / 441 1351 / 451
 TAT GAT GAG CAT ATT AAA AAT TAT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA
 tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys
 1381 / 461 1411 / 471
 TTC ATA AAA TCA TTG TTT GAC GAC AAT GAA ATT TTA CAG ATC GTG GAT
 phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp
 1441 / 481 1471 / 491
 GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT
 glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr

FIGURE 9D

APPLN. FILING DATE: APRIL 19, 2001
TITLE: PEPTIDE SEQUENCES SPECIFIC FOR THE
HEMOLYTIC STAGES OF P. FALCIPARUM BEE...
INVENTOR(S): CLAUDINE GUERIN-MARCHAND ET AL
APPLICATION SERIAL No: 010830-116 **SHEET 15 of 18**

LSN.3'STOP -> 1-phase Translation

DNA sequence 1482 b.p. CAAGAACAACAA ... ATGAAACTATAA linear

[illegible]

FIGURE 10A

361 / 121 391 / 131
 GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA
 glu gln gln ser asp leu glu gln glu arg ala lys glu lys leu gln glu gln gln
 421 / 141 451 / 151
 AGC GAT TTA GAA CAA GAG AGA CTT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA
 ser asp leu glu gln glu arg leu ala lys glu lys leu gln glu gln ser asp leu
 481 / 161 511 / 171
 GAA CAA GAG AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG
 glu gln glu arg ala lys glu lys leu gln glu gln ser asp leu glu gln glu
 541 / 181 571 / 191
 AGA CGT GCT AAA GAA AAG TTG CAA GAA CAA CAA AGC GAT TTA GAA CAA GAG AGA CGT GCT
 arg arg ala lys glu lys leu gln glu gln gln ser asp leu glu gln arg ala
 601 / 201 631 / 211
 AAA GAA AAG TTG CAA GAG CAG CAA CAA AGA GAT TTA GAA CAA AGG AAG GCT GAT ACG AAA AAA
 lys glu lys leu gln glu gln arg asp leu glu gln arg lys ala asp thr lys lys
 661 / 221 691 / 231
 AAT TTA GAA AGA AAA AAG AAG GAA CAA CAT GGA GAT ATA TTA GCA GAG GAT TTA TAT GGT CGT TTA
 asn leu glu arg lys lys glu his gly asp ile leu ala glu asp leu tyr gly arg leu
 721 / 241 751 / 251
 GAA ATA CCA GCT ATA GAA CTT CCA TCA GAA AAT GAA CGT GGA TAT TAT ATA CCA CAT CAA
 glu ile pro ala ile glu leu pro ser glu asn glu arg gly tyr ile pro his gln
 781 / 261 811 / 271
 TCT TCT TTA CCT CAG GAC AAC AGA GGG AAT AGT AGA GAT TCC AAG GAA ATA TCT ATA ATA
 ser ser leu pro gln asp asn arg gly asn ser arg asp ser lys glu ile ser ile ile

FIGURE 10B

| | | | | | | | | | | |
|------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| 841 / 281 | GAA AAA | ACA AAT | AGA GAA | TCT ATT | ACA ACA | AAT GTT | GAA GGA | CGA AGG | GAT ATA | CAT AAA |
| 901 / 301 | glu lys | thr asn | arg glu | ser ile | thr thr | asn val | glu gly | arg arg | asp ile | his lys |
| 961 / 321 | GGA CAT | CTT GAA | AAG AAG | AAA GAT | GGT TCA | ATA AAA | CCA GAA | CAA AAA | GAA GAT | AAA TCT |
| 961 / 321 | gly his | leu glu | glu lys | lys asp | gly ser | ile lys | pro glu | gln lys | glu asp | lys ser |
| 1021 / 341 | GCT GAC | ATA CAA | AAT CAT | ACA TTA | GAG ACA | GTA AAT | ATT TCT | GAT GAT | AAT GAT | TTT CAA |
| 1021 / 341 | ala asp | ile gln | asn his | thr thr | leu glu | val asn | ile ser | asp val | asn asp | phe gln |
| 1081 / 361 | ATA AGT | AAG TAT | GAG GAT | GAT ATA | AGT GCT | GAA TAT | GAC GAT | TCA TTA | ATA GAT | GAA GAA |
| 1081 / 361 | ile ser | lys tyr | glu asp | glu ile | ser ala | glu tyr | asp asp | ser leu | ile asp | glu glu |
| 1141 / 381 | GAA GAT | GAT GAA | GAC TTA | GAC GAA | TTT AAG | CCT ATT | GTG CAA | TAT GAC | AAT TTC | CAA GAT |
| 1141 / 381 | glu asp | asp glu | asp leu | asp glu | phe lys | pro ile | val gln | tyr asp | asn phe | gln asp |
| 1201 / 401 | GAA GAA | AAC ATA | GGA ATT | TAT AAA | GAA CTA | GAA GAT | TTG ATA | GAG AAA | AAT GAA | AAT TTA |
| 1201 / 401 | glu glu | asn ile | gly ile | tyr lys | glu leu | glu asp | leu ile | glu lys | asn glu | asn leu |
| 1261 / 421 | GAT GAT | TTA GAT | GAA GGA | ATA GAA | AAA TCA | TCA GAA | GAA TTA | TCT GAA | GAA AAA | ATA AAA |
| 1261 / 421 | asp asp | leu asp | glu gly | ile glu | lys ser | ser ser | glu leu | ser glu | glu lys | ile lys |
| 1261 / 421 | AAA GGA | AAG AAA | TAT GAA | AAA ACA | AAG GAT | AAT AAT | TTT AAA | CCA AAT | GAT AAA | AGT TTG |
| 1261 / 421 | lys gly | lys lys | tyr glu | lys thr | lys asp | asn phe | lys pro | asn asp | lys ser | leu |

FIGURE 10C

| | |
|---|------------|
| 1321 / 441 | 1351 / 451 |
| TAT GAT GAG CAT ATT AAA AAT GAT AAG CAG GTT AAT AAG GAA AAG GAA AAA | |
| tyr asp glu his ile lys lys tyr lys asn asp lys gln val asn lys glu lys glu lys | |
| 1381 / 461 | 1411 / 471 |
| TTC ATA AAA TCA TTG TTT CAT ATA TTT GAC GAA AAT GAA ATT TTA CAG ATC GTG GAT | |
| phe ile lys ser leu phe his ile phe asp gly asp asn glu ile leu gln ile val asp | |
| 1441 / 481 | 1471 / 491 |
| GAG TTA TCT GAA GAT ATA ACT AAA TAT TTT ATG AAA CTA TAA AAG GTT ATA TAT | |
| glu leu ser glu asp ile thr lys tyr phe met lys leu OCH lys val ile tyr | |

FIGURE 10D